FIG. 1

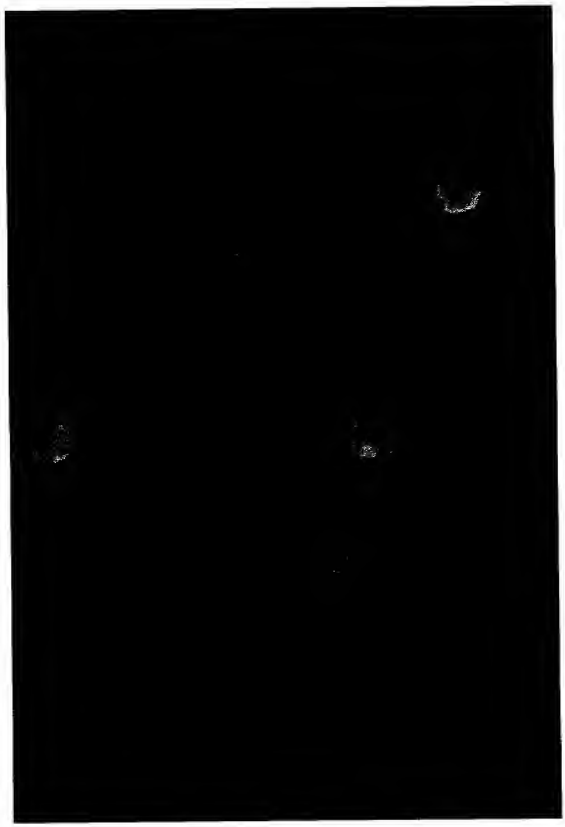

FIG. 2

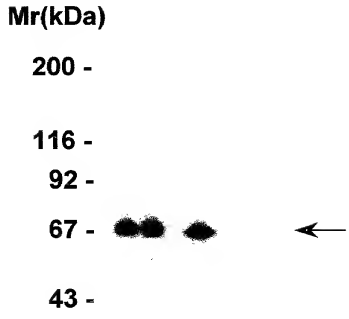
Mr(kDa)
200 -
116 -
92 -
67 -
43 -
1 2 3 4

FIG. 3

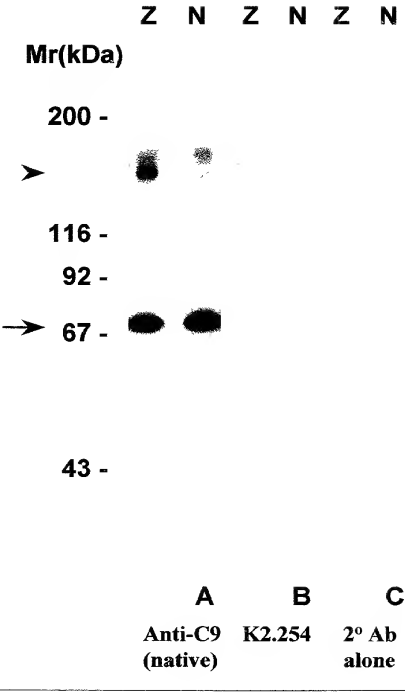
Z N Z N Z N
Mr(kDa)
200 -
116 -
92 -
67 -
43 -
A B C
Anti-C9 (native)
K2.254
2° Ab alone

FIG. 4

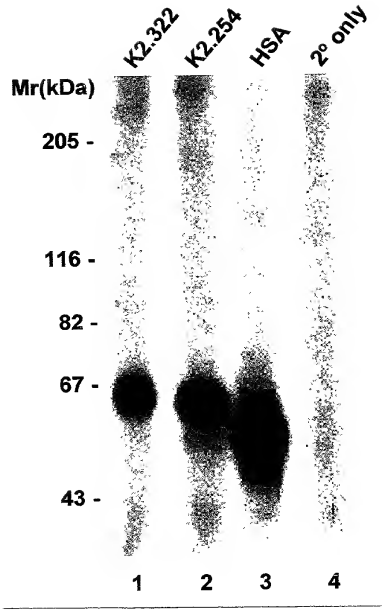

FIG. 5

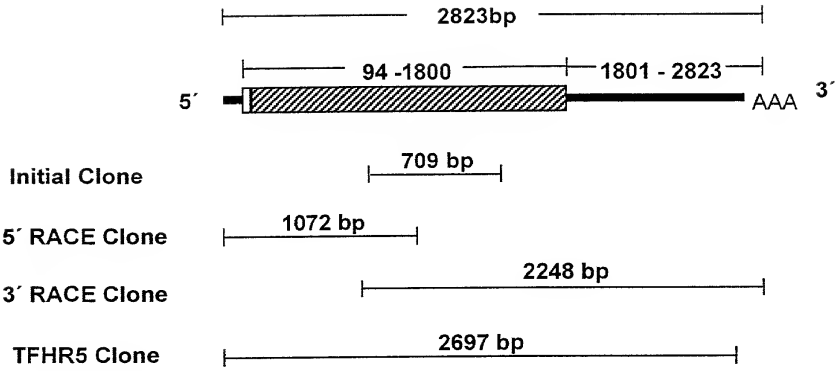
2823bp
94 -1800
1801 - 2823
5´
AAA
3´
Initial Clone
709 bp
5´ RACE Clone
1072 bp
3´ RACE Clone
2248 bp
TFHR5 Clone
2697 bp

FIG. 6

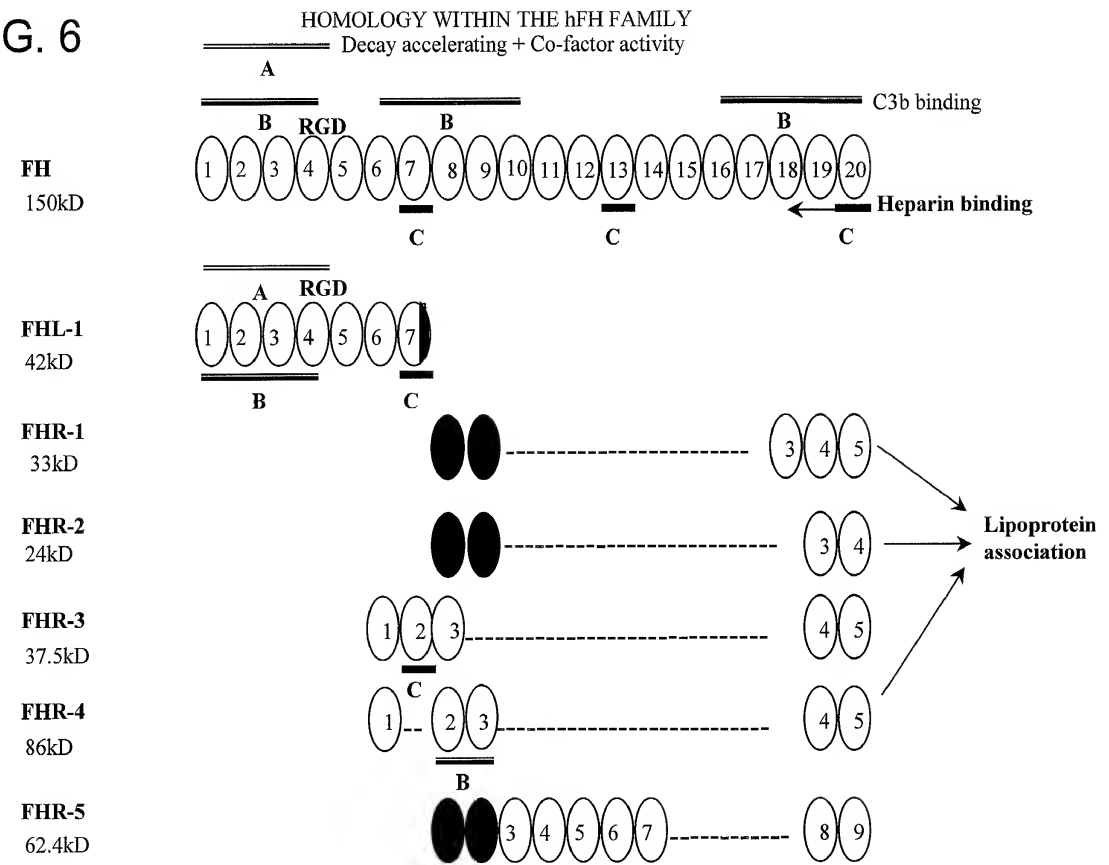
HOMOLOGY WITHIN THE hFH FAMILY
Decay accelerating + Co-factor activity
A
B
RGD
B
B
C3b binding
FH
150kD
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Heparin binding
C
C
C
A
RGD
FHL-1
42kD
1 2 3 4 5 6 7
B
C
FHR-1
33kD
3 4 5
FHR-2
24kD
3 4
Lipoprotein association
FHR-3
37.5kD
1 2 3
4 5
C
FHR-4
86kD
1 2 3
4 5
B
FHR-5
62.4kD
3 4 5 6 7
8 9

FIG. 6A

CAP Protein
(2823bp/569AA)

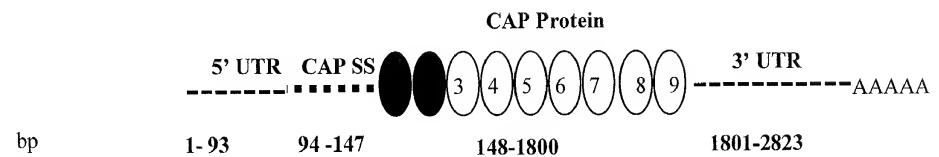

FIG. 7

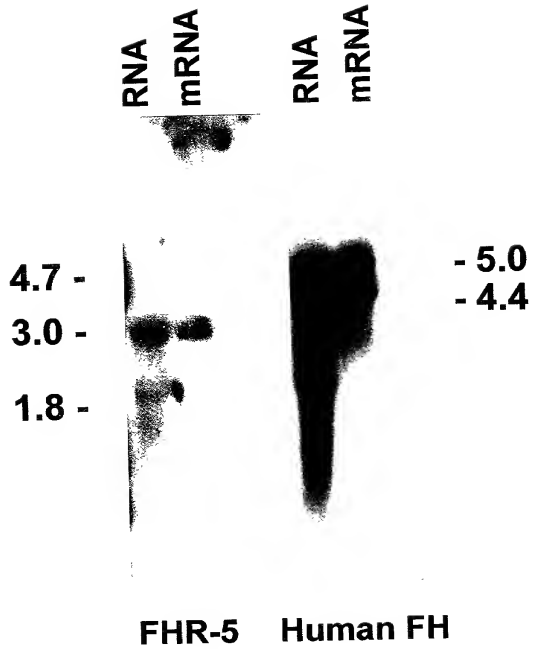
RNA
mRNA
RNA
mRNA
4.7 -
3.0 -
1.8 -
- 5.0
- 4.4
FHR-5
Human FH

FIG. 8

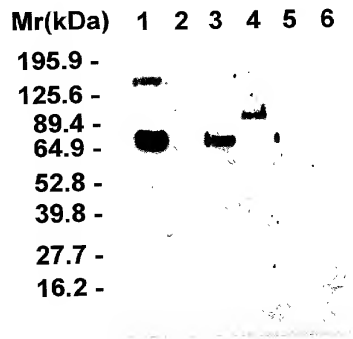
Mr(kDa)
1
2
3
4
5
6
195.9 -
125.6 -
89.4 -
64.9 -
52.8 -
39.8 -
27.7 -
16.2 -

FIG. 9

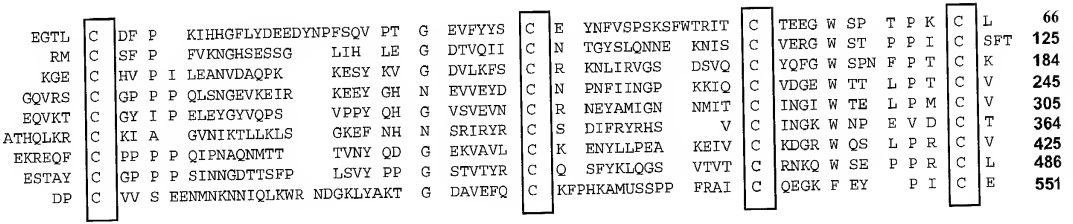
EGTL C DF P KIHHGFLYDEEDYNPFSQV PT G EVFYYS C E YNFVSPSKSFWTRIT C TEEG W SP T P K C L 66
RM C SF P FVKNGHSESSG LIH LE G DTVQII C N TGYSLQNNE KNIS C VERG W ST P P I C SFT 125
KGE C HV P I LEANVDAQPK KESY KV G DVLKFS C R KNLIRVGS DSVQ C YQFG W SPN F P T C K 184
GQVRS C GP P P QLSNGEVKEIR KEEY GH N EVVEYD C N PNFIINGP KKIQ C VDGE W TT L P T C V 245
EQVKT C GY I P ELEYGYVQPS VPPY QH G VSVEVN C R NEYAMIGN NMIT C INGI W TE L P M C V 305
ATHQLKR C KI A GVNIKTLLKLS GKEF NH N SRIRYR C S DIFRYRHS V C INGK W NP E V D C T 364
EKREQF C PP P P QIPNAQNMTT TVNY QD G EKVAVL C K ENYLLPEA KEIV C KDGR W QS L P R C V 425
ESTAY C GP P P SINNGDTTSFP LSVY PP G STVTYR C Q SFYKLQGS VTVT C RNKQ W SE P P R C L 486
DP C VV S EENMNKNNIQLKWR NDGKLYAKT G DAVEFQ C KFPHKAMUSSPP FRAI C QEGK F EY P I C E 551
Amino Acid Coordinates

FIG. 10

FHR-5	SCR	1	EGTLCDFPKIHHGFLYDEEDYNPFSQVPTGEVFYYSCEYNFVSPSKSFWTRITCTEEGWSPTPKCL	% Homology
FHR-1	SCR	1	A F N - K K N	89 4%
FHR-2	SCR	1	AMF N - K K A	87 9%
FHR-5	SCR	2	RMCSFPFVKNGHSESSGLIHLEGDTVQIICNTGYSLQNNEKNISCVERGWSTPPICSFT	
FHR-1	SCR	2	L F E QT R N K RS	83 0%
FHR-2	SCR	2	L F E QT R N K RS	83 0%
FHR-5	SCR	3	KGECHVPILEANVDAQPKKESYKVGDVLKFSCRKNLIRVGSDSVQCYQFGWSPNFPTCK	
FH	SCR	10	ER EL KIDVHLVPDR DQY E KPGFTI PNS H L DL I	47 5%
FHR-5	SCR	4	GQVRSCGPPPQLSNGEVKEIRKEEYGHNEVVEYDCNPNFIINGPKKIQCVDGEWTTLPTCV	
FH	SCR	11	E Q E L N KT S Y R LMK N V I 73 8%	
FHR-5	SCR	5	EQVKTCGYIPELEYGYVQPSVPPYQHGVSVEVNCRNEYAMIGNNMITCINGIWTELPMCV	
FH	SCR	12	VEES D H WA L S YY D F SESFT HRS H V Q Q	56 7%
FHR-5	SCR	6	ATHQLKRCKIAGVNIKTLLKLSGKEFNHNSRIRYRCSDIFRYRHSVCINGKWNPEVDCT	
FH	SCR	13	IDK K SSNLI LEEHLKNK D N RGKEGWI T R D N S	47 5%
FHR-5	SCR	7	EKREQFCPPPQIPNAQNMTTTVNYQDGEKVAVLCKENYLLPEAKEIVCKDGRWQSLPRCV	
FH	SCR	14	MAQI L SH L R S Q IQ GE T I L	70 5
FHR-5	SCR	8	ESTAYCG-PPPSINNGDTTSFPLSVYPPGSTVTYRCQSFYKLQGSVTVTCRNKQWSEPPRCL	
FH	SCR	19	D GK - PID I A A S E Q NL Q E NKRI G K	67 2%
FHR-1	SCR	4	D GK - PID I A A S E Q NL Q E NKRI G K	62 3%
FHR-2	SCR	3	I AE G PID I L A S E Q NL Q E NNQI G K	63 9%
FHR-3	SCR	4	N SEK - PIS L K V Q R E Q Y E NY S GE A I	65 6%
FHR-4	SCR	4	N SEK - PIS L K V Q R E Q Y E NY S GE I	63 9%
FHR-5	SCR	9	DPCVVSEENNMNKNMQLKWRNDGKLYAKTGDAVEFQCKFPHKAMISSPPFRAICQEGKFEYPICE	
FH	SCR	20	H I R I - ENY A RWTAKQ SR ES V RGYRLSSRSHTL TT WD L T AKR	41 8%
FHR-1	SCR	5	H I R I - ENY A RWTAKQ LR ESAEFV RGYRLSSRSHTL TT WD L T AKR	41 7%
FHR-2	SCR	4	D I Q I - EKY K KWT KQ SR I V RGYHPTKS-HS AM N LV S EK	55 2%
FHR-3	SCR	5	H IIT - K G S R Y TIEFM LGYN NTS-LS Q V R IV R	58 5%
FHR-4	SCR	5	H IIT - QLKGKS I Y TIEFM LGYN NTSVLS Q V R IV R	58 5%

FIG. 11A

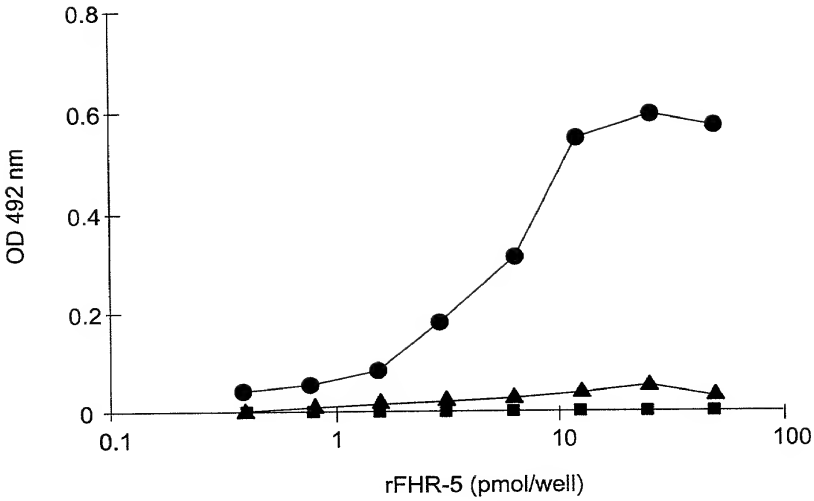

FIG. 11B